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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/10/010,568

DATE: 12/20/2001
 TIME: 13:49:07

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ENTERED

3 <110> APPLICANT: Bristol-Myers Squibb Company
 5 <120> TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY23,
 EXPRESSED HIGHLY IN
 6 KIDNEY
 8 <130> FILE REFERENCE: D0077 NP
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/010,568
 C--> 10 <141> CURRENT FILING DATE: 2001-12-07
 10 <150> PRIOR APPLICATION NUMBER: US 60/251,926
 11 <151> PRIOR FILING DATE: 2000-12-07
 13 <150> PRIOR APPLICATION NUMBER: US 60/269,795
 14 <151> PRIOR FILING DATE: 2001-02-14
 16 <160> NUMBER OF SEQ ID NOS: 55
 18 <170> SOFTWARE: PatentIn version 3.0
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 1081
 22 <212> TYPE: DNA
 23 <213> ORGANISM: homo sapiens
 25 <220> FEATURE:
 26 <221> NAME/KEY: CDS
 27 <222> LOCATION: (54)..(1064)
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 31 Met
 32 1
 34 aat gag cca cta gac tat tta gca aat gct tct gat ttc ccc gat tat 104
 35 Asn Glu Pro Leu Asp Tyr Leu Ala Asn Ala Ser Asp Phe Pro Asp Tyr
 36 5 10 15
 38 gca gct gct ttt gga aat tgc act gat gaa aac atc cca ctc aag atg 152
 39 Ala Ala Ala Phe Gly Asn Cys Thr Asp Glu Asn Ile Pro Leu Lys Met
 40 20 25 30
 42 cac tac ctc cct gtt att tat ggc att atc ttc ctc gtg gga ttt cca 200
 43 His Tyr Leu Pro Val Ile Tyr Gly Ile Ile Phe Leu Val Gly Phe Pro
 44 35 40 45
 46 ggc aat gca gta gtg ata tcc act tac att ttc aaa atg aga cct tgg 248
 47 Gly Asn Ala Val Val Ile Ser Thr Tyr Ile Phe Lys Met Arg Pro Trp
 48 50 55 60 65
 50 aag agc agc acc atc att atg ctg aac ctg gcc tgc aca gat ctg ctg 296
 51 Lys Ser Ser Thr Ile Ile Met Leu Asn Leu Ala Cys Thr Asp Leu Leu
 52 70 75 80
 54 tat ctg acc agc ctc ccc ttc ctg att cac tac tat gcc agt ggc gaa 344
 55 Tyr Leu Thr Ser Leu Pro Phe Leu Ile His Tyr Tyr Ala Ser Gly Glu
 56 85 90 95
 58 aac tgg atc ttt gga gat ttc atg tgt aag ttt atc cgc ttc agc ttc 392
 59 Asn Trp Ile Phe Gly Asp Phe Met Cys Lys Phe Ile Arg Phe Ser Phe
 60 100 105 110
 62 cat ttc aac ctg tat agc agc atc ctc ttc ctc acc tgt ttc agc atc 440
 63 His Phe Asn Leu Tyr Ser Ser Ile Leu Phe Leu Thr Cys Phe Ser Ile
 64 115 120 125

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66 ttc cgc tac tgt gtg atc att cac cca atg agc tgc ttt tcc att cac      488
67 Phe Arg Tyr Cys Val Ile Ile His Pro Met Ser Cys Phe Ser Ile His
68 130                               135                               140                               145
70 aaa act cga tgt gca gtt gta gcc tgt gct gtg gtg tgg atc att tca      536
71 Lys Thr Arg Cys Ala Val Val Ala Cys Ala Val Val Trp Ile Ile Ser
72                               150                               155                               160
74 ctg gta gct gtc att ccg atg acc ttc ttg atc aca tca acc aac agg      584
75 Leu Val Ala Val Ile Pro Met Thr Phe Leu Ile Thr Ser Thr Asn Arg
76                               165                               170                               175
78 acc aac aga tca gcc tgt ctc gac ctc acc agt tcg gat gaa ctc aat      632
79 Thr Asn Arg Ser Ala Cys Leu Asp Leu Thr Ser Ser Asp Glu Leu Asn
80                               180                               185                               190
82 act att aag tgg tac aac ctg att ttg act gca act act ttc tgc ctc      680
83 Thr Ile Lys Trp Tyr Asn Leu Ile Leu Thr Ala Thr Thr Phe Cys Leu
84                               195                               200                               205
86 ccc ttg gtg ata gtg aca ctt tgc tat acc acg att atc cac act ctg      728
87 Pro Leu Val Ile Val Thr Leu Cys Tyr Thr Thr Ile Ile His Thr Leu
88 210                               215                               220                               225
90 acc cat gga ctg caa act gac agc tgc ctt aag cag aaa gca cga agg      776
91 Thr His Gly Leu Gln Thr Asp Ser Cys Leu Lys Gln Lys Ala Arg Arg
92                               230                               235                               240
94 cta acc att ctg cta ctc ctt gca ttt tac gta tgt ttt tta ccc ttc      824
95 Leu Thr Ile Leu Leu Leu Leu Ala Phe Tyr Val Cys Phe Leu Pro Phe
96                               245                               250                               255
98 cat atc ttg agg gtc att cgg atc gaa tct cgc ctg ctt tca atc agt      872
99 His Ile Leu Arg Val Ile Arg Ile Glu Ser Arg Leu Leu Ser Ile Ser
100                               260                               265                               270
102 tgt tcc att gag aat cag atc cat gaa gct tac atc gtt tct aga cca      920
103 Cys Ser Ile Glu Asn Gln Ile His Glu Ala Tyr Ile Val Ser Arg Pro
104                               275                               280                               285
106 tta gct gct ctg aac acc ttt ggt aac ctg tta cta tat gtg gtg gtc      968
107 Leu Ala Ala Leu Asn Thr Phe Gly Asn Leu Leu Leu Tyr Val Val Val
108 290                               295                               300                               305
110 agc gac aac ttt cag cag gct gtc tgc tca aca gtg aga tgc aaa gta      1016
111 Ser Asp Asn Phe Gln Gln Ala Val Cys Ser Thr Val Arg Cys Lys Val
112                               310                               315                               320
114 agc ggg aac ctt gag caa gca aag aaa att agt tac tca aac aac cct      1064
115 Ser Gly Asn Leu Glu Gln Ala Lys Lys Ile Ser Tyr Ser Asn Asn Pro
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122 <211> LENGTH: 337
123 <212> TYPE: PRT
124 <213> ORGANISM: homo sapiens
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129 1                               5                               10                               15
132 Tyr Ala Ala Ala Phe Gly Asn Cys Thr Asp Glu Asn Ile Pro Leu Lys
133                               20                               25                               30

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136 Met His Tyr Leu Pro Val Ile Tyr Gly Ile Ile Phe Leu Val Gly Phe
137          35          40          45
140 Pro Gly Asn Ala Val Val Ile Ser Thr Tyr Ile Phe Lys Met Arg Pro
141          50          55          60
144 Trp Lys Ser Ser Thr Ile Ile Met Leu Asn Leu Ala Cys Thr Asp Leu
145 65          70          75          80
148 Leu Tyr Leu Thr Ser Leu Pro Phe Leu Ile His Tyr Tyr Ala Ser Gly
149          85          90          95
152 Glu Asn Trp Ile Phe Gly Asp Phe Met Cys Lys Phe Ile Arg Phe Ser
153          100          105          110
156 Phe His Phe Asn Leu Tyr Ser Ser Ile Leu Phe Leu Thr Cys Phe Ser
157          115          120          125
160 Ile Phe Arg Tyr Cys Val Ile Ile His Pro Met Ser Cys Phe Ser Ile
161          130          135          140
164 His Lys Thr Arg Cys Ala Val Val Ala Cys Ala Val Val Trp Ile Ile
165 145          150          155          160
168 Ser Leu Val Ala Val Ile Pro Met Thr Phe Leu Ile Thr Ser Thr Asn
169          165          170          175
172 Arg Thr Asn Arg Ser Ala Cys Leu Asp Leu Thr Ser Ser Asp Glu Leu
173          180          185          190
176 Asn Thr Ile Lys Trp Tyr Asn Leu Ile Leu Thr Ala Thr Thr Phe Cys
177          195          200          205
180 Leu Pro Leu Val Ile Val Thr Leu Cys Tyr Thr Thr Ile Ile His Thr
181          210          215          220
184 Leu Thr His Gly Leu Gln Thr Asp Ser Cys Leu Lys Gln Lys Ala Arg
185 225          230          235          240
188 Arg Leu Thr Ile Leu Leu Leu Leu Ala Phe Tyr Val Cys Phe Leu Pro
189          245          250          255
192 Phe His Ile Leu Arg Val Ile Arg Ile Glu Ser Arg Leu Leu Ser Ile
193          260          265          270
196 Ser Cys Ser Ile Glu Asn Gln Ile His Glu Ala Tyr Ile Val Ser Arg
197          275          280          285
200 Pro Leu Ala Ala Leu Asn Thr Phe Gly Asn Leu Leu Leu Tyr Val Val
201          290          295          300
204 Val Ser Asp Asn Phe Gln Gln Ala Val Cys Ser Thr Val Arg Cys Lys
205 305          310          315          320
208 Val Ser Gly Asn Leu Glu Gln Ala Lys Lys Ile Ser Tyr Ser Asn Asn
209          325          330          335
212 Pro
216 <210> SEQ ID NO: 3
217 <211> LENGTH: 362
218 <212> TYPE: PRT
219 <213> ORGANISM: GALLUS GALLUS
221 <400> SEQUENCE: 3
223 Met Thr Glu Ala Leu Ile Ser Ala Ala Leu Asn Gly Thr Gln Pro Glu
224 1          5          10          15
226 Leu Leu Ala Gly Gly Trp Ala Ala Gly Asn Ala Thr Thr Lys Cys Ser
227          20          25          30
229 Leu Thr Lys Thr Gly Phe Gln Phe Tyr Tyr Leu Pro Thr Val Tyr Ile

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230          35          40          45
232 Leu Val Phe Ile Thr Gly Phe Leu Gly Asn Ser Val Ala Ile Trp Met
233          50          55          60
235 Phe Val Phe His Met Arg Pro Trp Ser Gly Ile Ser Val Tyr Met Phe
236 65          70          75          80
238 Asn Leu Ala Leu Ala Asp Phe Leu Tyr Val Leu Thr Leu Pro Ala Leu
239          85          90          95
241 Ile Phe Tyr Tyr Phe Asn Lys Thr Asp Trp Ile Phe Gly Asp Val Met
242          100          105          110
244 Cys Lys Leu Gln Arg Phe Ile Phe His Val Asn Leu Tyr Gly Ser Ile
245          115          120          125
247 Leu Phe Leu Thr Cys Ile Ser Val His Arg Tyr Thr Gly Val Val His
248          130          135          140
250 Pro Leu Lys Ser Leu Gly Arg Leu Lys Lys Lys Asn Ala Val Tyr Val
251 145          150          155          160
253 Ser Ser Leu Val Trp Ala Leu Val Val Ala Val Ile Ala Pro Ile Leu
254          165          170          175
256 Phe Tyr Ser Gly Thr Gly Val Arg Arg Asn Lys Thr Ile Thr Cys Tyr
257          180          185          190
259 Asp Thr Thr Ala Asp Glu Tyr Leu Arg Ser Tyr Phe Val Tyr Ser Met
260          195          200          205
262 Cys Thr Thr Val Phe Met Phe Cys Ile Pro Phe Ile Val Ile Leu Gly
263          210          215          220
265 Cys Tyr Gly Leu Ile Val Lys Ala Leu Ile Tyr Lys Asp Leu Asp Asn
266 225          230          235          240
268 Ser Pro Leu Arg Arg Lys Ser Ile Tyr Leu Val Ile Ile Val Leu Thr
269          245          250          255
271 Val Phe Ala Val Ser Tyr Leu Pro Phe His Val Met Lys Thr Leu Asn
272          260          265          270
274 Leu Arg Ala Arg Leu Asp Phe Gln Thr Pro Gln Met Cys Ala Phe Asn
275          275          280          285
277 Asp Lys Val Tyr Ala Thr Tyr Gln Val Thr Arg Gly Leu Ala Ser Leu
278          290          295          300
280 Asn Ser Cys Val Asp Pro Ile Leu Tyr Phe Leu Ala Gly Asp Thr Phe
281 305          310          315          320
283 Arg Arg Arg Leu Ser Arg Ala Thr Arg Lys Ser Ser Arg Arg Ser Glu
284          325          330          335
286 Pro Asn Val Gln Ser Lys Ser Glu Glu Met Thr Leu Asn Ile Leu Thr
287          340          345          350
289 Glu Tyr Lys Gln Asn Gly Asp Thr Ser Leu
290          355          360
292 <210> SEQ ID NO: 4
293 <211> LENGTH: 362
294 <212> TYPE: PRT
295 <213> ORGANISM: MELEAGRIS GALLOPAVO
297 <400> SEQUENCE: 4
299 Met Thr Glu Ala Leu Ile Ser Ala Ala Leu Asn Gly Thr Gln Pro Glu
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302 Leu Leu Ala Gly Gly Trp Ala Ala Gly Asn Ala Ser Thr Lys Cys Ser

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303          20          25          30
305 Leu Thr Lys Thr Gly Phe Gln Phe Tyr Tyr Leu Pro Thr Val Tyr Ile
306          35          40          45
308 Leu Val Phe Ile Thr Gly Phe Leu Gly Asn Ser Val Ala Ile Trp Met
309          50          55          60
311 Phe Val Phe His Met Arg Pro Trp Ser Gly Ile Ser Val Tyr Met Phe
312 65          70          75          80
314 Asn Leu Ala Leu Ala Asp Phe Leu Tyr Val Leu Thr Leu Pro Ala Leu
315          85          90          95
317 Ile Phe Tyr Tyr Phe Asn Lys Thr Asp Trp Ile Phe Gly Asp Val Met
318          100         105         110
320 Cys Lys Leu Gln Arg Phe Ile Phe His Val Asn Leu Tyr Gly Ser Ile
321          115         120         125
323 Leu Phe Leu Thr Cys Ile Ser Val His Arg Tyr Thr Gly Val Val His
324          130         135         140
326 Pro Leu Lys Ser Leu Gly Arg Leu Lys Lys Lys Asn Ala Val Tyr Val
327 145          150         155         160
329 Ser Ser Leu Val Trp Ala Leu Val Val Ala Val Ile Ala Pro Ile Leu
330          165         170         175
332 Phe Tyr Ser Gly Thr Gly Val Arg Arg Asn Lys Thr Ile Thr Cys Tyr
333          180         185         190
335 Asp Thr Thr Ala Asp Glu Tyr Leu Arg Ser Tyr Phe Val Tyr Ser Met
336          195         200         205
338 Cys Thr Thr Val Phe Met Phe Cys Ile Pro Phe Ile Val Ile Leu Gly
339          210         215         220
341 Cys Tyr Gly Leu Ile Val Lys Ala Leu Ile Tyr Lys Asp Leu Asp Asn
342 225          230         235         240
344 Ser Pro Leu Arg Arg Lys Ser Ile Tyr Leu Val Ile Ile Val Leu Thr
345          245         250         255
347 Val Phe Ala Val Ser Tyr Leu Pro Phe His Val Met Lys Thr Leu Asn
348          260         265         270
350 Leu Arg Ala Arg Leu Asp Phe Gln Thr Pro Gln Met Cys Ala Phe Asn
351          275         280         285
353 Asp Lys Val Tyr Ala Thr Tyr Gln Val Thr Arg Gly Leu Ala Ser Leu
354          290         295         300
356 Asn Ser Cys Val Asp Pro Ile Leu Tyr Phe Leu Ala Gly Asp Thr Phe
357 305          310         315         320
359 Arg Arg Arg Leu Ser Arg Ala Thr Arg Lys Ser Ser Arg Arg Ser Glu
360          325         330         335
362 Pro Asn Val Gln Ser Lys Ser Glu Glu Met Thr Leu Asn Ile Leu Thr
363          340         345         350
365 Glu Tyr Lys Gln Asn Gly Asp Thr Ser Leu
366          355         360
368 <210> SEQ ID NO: 5
369 <211> LENGTH: 373
370 <212> TYPE: PRT
371 <213> ORGANISM: MUS MUSCULUS
373 <400> SEQUENCE: 5
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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/010,568

DATE: 12/20/2001

TIME: 13:49:08

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